RAW SEQUENCE LISTING   DATE: 01/30/2002
PATENT APPLICATION: US/10/035,060   TIME: 18:05:01

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Output Set: N:\CRF3\01302002\J035060.raw

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 1 <110> APPLICANT: Edwards, David
 2        Wong, Siu-Yin
 3        Herrnstadt, Corinna
 4        Wilcox, Edward
 5 <120> TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
 6        Toxicity Of
 7        Bacillus Thuringiensis Lepidoteran Toxins, and Recombinant DNA Sequences
 8        Therefor
 9 <130> FILE REFERENCE: M12C1FDF3D1
10 <140> CURRENT APPLICATION NUMBER: 10/035,060
11 <141> CURRENT FILING DATE: 2001-12-27
13 <150> PRIOR APPLICATION NUMBER: 09/405,788
14 <151> PRIOR FILING DATE: 1999-09-27
17 <150> PRIOR APPLICATION NUMBER: US 08/580,781
18 <151> PRIOR FILING DATE: 1995-12-29
19 <150> PRIOR APPLICATION NUMBER: US 08/420,615
20 <151> PRIOR FILING DATE: 1995-04-10
21 <150> PRIOR APPLICATION NUMBER: US 08/097,808
22 <151> PRIOR FILING DATE: 1993-07-27
23 <150> PRIOR APPLICATION NUMBER: US 07/980,128
24 <151> PRIOR FILING DATE: 1992-11-23
25 <150> PRIOR APPLICATION NUMBER: US 07/803,920
26 <151> PRIOR FILING DATE: 1991-12-06
27 <150> PRIOR APPLICATION NUMBER: US 07/356,599
28 <151> PRIOR FILING DATE: 1989-05-24
29 <150> PRIOR APPLICATION NUMBER: US 06/904,572
30 <151> PRIOR FILING DATE: 1986-09-05
31 <150> PRIOR APPLICATION NUMBER: US 06/808,129
32 <151> PRIOR FILING DATE: 1985-12-12
33 <160> NUMBER OF SEQ ID NOS: 9
34 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 3537
38 <212> TYPE: DNA
39 <213> ORGANISM: Bacillus Thuringiensis
40 <400> SEQUENCE: 1
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43        tcgctaacgc aatttctttt gagtgaattt gttcccggtg ctggatttgt gttaggacta     180
44        gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttcc tgtacaaatt     240
45        gaacagttaa ttaaccaaag aatagaagaa ttcgctagga ccaagccat ttctagatta      300
46        gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat     360
47        cctactaatc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc     420
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50     aggtgggggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt   600
51     ggcaactata cagattatgc tgtgcgctgg tacaatacgg gattagagcg tgtatgggga    660
52     ccggattcta gagattgggt aaggtataat caatttagaa gagagctaac acttactgta    720
53     ttagatatcg ttgctctatt ctcaaattat gatagtcgaa ggtatccaat tcgaacagtt    780
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56     aatagtataa ccatttatac tgatgtgcat agaggcttta attattggtc agggcatcaa    960
57     ataacagctt ctcctgtagg gtttttcagga ccagaattcg cattcccttt atttgggaat   1020
58     gcggggaatg cagctccacc cgtacttgtc tcattaactg gtttgggggat ttttagaaca   1080
59     ttatcttcac ctttatatag aagaattata cttggttcag gcccaaataa tcaggaactg    1140
60     tttgtccttg atggaacgga gtttttctttt gcctccctaa cgaccaactt gccttccact    1200
61     atatatagac aaaggggtac agtcgattca ctagatgtaa taccgccaca ggataatagt    1260
62     gtaccacctc gtgcgggatt tagccatcga ttgagtcatg ttacaatgct gagccaagca    1320
63     gctggagcag tttacacctt gagagctcaa cgtcctatgt tctcttggat acatcgtagt    1380
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68     cacctcaacg ttaattgggg taattcatcc attttttcca atacagtacc agctacagct    1680
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76     gggtggggcg gaagtacagg gattaccatc caaggagggg atgacgtatt taaagaaaat    2160
77     tacgtcacac tatcaggtac ctttgatgag tgctatccaa catatttgta tcaaaaaatc    2220
78     gatgaatcaa aattaaaagc ctttacccgt tatcaattaa gagggtatat cgaagatagt    2280
79     caagacttag aaatctattt aattcgctac aatgcaaaac atgaaacagt aaatgtgcca    2340
80     ggtacggggtt ccttatggcc gctttcagcc caaagtccaa tcggaaagtg tggagagccg    2400
81     aatcgatgcg cgccacacct tgaatggaat cctgacttag attgttcgtg tagggatgga    2460
82     gaaaagtgtg cccatcattc gcatcatttc tccttagaca ttgatgtagg atgtacagac    2520
83     ttaaatgagg acctaggtgt atgggtgatc tttaagatta agacgcaaga tgggcacgca    2580
84     agactaggga atctagagtt tctcgaagag aaaccattag taggagaagc gctagctcgt    2640
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87     caattacaag cggatacgaa tattgccatg attcatgcgg cagataaacg tgttcatagc    2820
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91     gaagaacaaa acaaccaacg ttcggtcctt gttgttccgg aatgggaagc agaagtgtca    3060
92     caagaagttc gtgtctgtcc gggtcgtggc tatatccttc gtgtcacagc gtacaaggag    3120
93     ggatatggag aaggttgcgt aaccattcat gagatcgaga acaatacaga cgaactgaag    3180
94     tttagcaact gcgtagaaga ggaaatctat ccaaataaca cggtaacgtg taatgattat    3240
95     actgtaaatc aagaagaata cggaggtgcg tacacttctc gtaatcgagg atataacgaa    3300
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98       ggttatgtga caaaagaatt agaatacttc ccagaaaccg ataaggtatg gattgagatt    3480
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102 <211> LENGTH: 1177
103 <212> TYPE: PRT
104 <213> ORGANISM: Bacillus Thuringiensis
105 <400> SEQUENCE: 2
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109                  20                  25                  30
110      Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
111                  35                  40                  45
112      Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
113          50                  55                  60
114      Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
115      65                  70                  75                  80
116      Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
117                      85                  90                  95
118      Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
119                  100                 105                 110
120      Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
121              115                 120                 125
122      Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
123          130                 135                 140
124      Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
125      145                 150                 155                 160
126      Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
127                      165                 170                 175
128      Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
129                  180                 185                 190
130      Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
131                  195                 200                 205
132      Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
133          210                 215                 220
134      Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
135      225                 230                 235                 240
136      Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
137                  245                 250                 255
138      Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
139                  260                 265                 270
140      Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
141                  275                 280                 285
142      Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
143          290                 295                 300
144      Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Tyr Trp Ser Gly His Gln
145      305                 310                 315                 320
146      Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
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147                     325              330              335
148     Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
149                     340              345              350
150     Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
151                 355              360              365
152     Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
153             370              375              380
154     Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
155     385              390              395              400
156     Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
157                 405              410              415
158     Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
159                 420              425              430
160     Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
161             435              440              445
162     Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
163         450              455              460
164     Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
165     465              470              475              480
166     Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
167                 485              490              495
168     Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
169                 500              505              510
170     Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
171             515              520              525
172     Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
173         530              535              540
174     Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
175     545              550              555              560
176     Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
177             565              570              575
178     Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
179             580              585              590
180     Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
181         595              600              605
182     Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
183         610              615              620
184     Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
185     625              630              635              640
186     Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
187             645              650              655
188     Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
189             660              665              670
190     His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
191         675              680              685
192     Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
193         690              695              700
194     Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
195     705              710              715              720
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198    Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
199                    740             745             750
200    Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
201                    755             760             765
202    Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
203        770             775             780
204    Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
205    785             790             795                 800
206    Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
207                805             810             815
208    Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
209                820             825             830
210    Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
211                835             840             845
212    Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
213        850             855             860
214    Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
215    865             870             875             880
216    Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
217                885             890             895
218    Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
219                900             905             910
220    Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
221        915             920             925
222    Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
223        930             935             940
224    Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
225    945             950             955             960
226    Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
227                965             970             975
228    Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
229                980             985             990
230    Lys Gly His Val Asp Val Glu Glu  Gln Asn Asn Gln Arg  Ser Val Leu
231                995             1000            1005
232    Val Leu  Pro Glu Trp Glu Ala  Glu Val Ser Gln Glu  Val Arg Val
233        1010            1015            1020
234    Cys Pro  Gly Arg Gly Tyr Ile  Leu Arg Val Thr Ala  Tyr Lys Glu
235        1025            1030            1035
236    Gly Tyr  Gly Glu Gly Cys Val  Thr Ile His Glu Ile  Glu Asn Asn
237        1040            1045            1050
238    Thr Asp  Glu Leu Lys Phe Ser  Asn Cys Val Glu Glu  Glu Ile Tyr
239        1055            1060            1065
240    Pro Asn  Asn Thr Val Thr Cys  Asn Asp Tyr Thr Val  Asn Gln Glu
241        1070            1075            1080
242    Glu Tyr  Gly Gly Ala Tyr Thr  Ser Arg Asn Arg Gly  Tyr Asn Glu
243        1085            1090            1095
244    Ala Pro  Ser Val Pro Ala Asp  Tyr Ala Ser Val Tyr  Glu Glu Lys
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